

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-62 as originally filed in PCT/IN2003/000204 (canceled)

Claims 1-61 as amended under Article 19 (canceled)

Claims 1-56 as amended under Article 34 (canceled)

63. (Previously Presented) A simple and improved method of detection and/or quantitation of target nucleic acid sequence comprising (i) providing at least two oligonucleotides as a pair of primers for amplification of said target sequence; (ii) subjecting the target sequence to amplification such that the 3' ends of said pair of primers are on two opposite strands and separated from one another by 0-25 nucleotide pairs in the final amplification product; and (iii) carrying out denaturation step and at least a selective annealing step in each cycle.

64. (Previously Presented) The method of claim 63 wherein said denaturation carried out is less than 20 seconds preferably less than 10 seconds, said annealing carried out is less than 15 seconds preferably less than 5 seconds and extension of less than 10 seconds preferably 0 seconds in each cycle for high through put PCR or nucleic acid target analysis.

65. (Previously Presented) The method of claim 63 wherein one of the two oligonucleotides of the nucleic acid amplification reaction is labeled at or near preferably near 3'end with a fluorescent or luminescent signaling moiety kept quenched when the labeled oligonucleotide is not incorporated into the amplification product, the same labeled oligonucleotide, when incorporated into the amplification product adapted to generate signal through removal of quenching by separating quencher from the signaling moiety.

66. (Previously Presented) The method of claim 63 wherein a first oligonucleotide is labeled with a donor MET moiety at or near preferably near 3' end preferably within 2-10

nucleotides away from 3' end and the second oligonucleotide is labeled with an acceptor MET moiety, at or near preferably near 3' end within 2-10 nucleotides away from 3' end, the said donor and acceptor MET moieties belonging to a molecular energy transfer pair and so configured that the donor and the acceptor moieties come within MET distance, 10–80 Angstrom or the nucleotides to which the MET moieties are attached are separated by 2–20 nucleotides preferably by 4 – 12 nucleotides.

67. (Previously Presented) The method of claim 66 wherein the labeled oligonucleotides are selected from linear, hair-pin or otherwise configuration.

68. (Previously Presented) The method of claim 66 wherein the oligonucleotide labeled with the acceptor moiety or both the oligonucleotides labeled separately with donor or acceptor moiety are provided in quenched condition with quencher or quenchers or by providing them with hair-pin stem structure such that the emission energy of the acceptor or both the acceptor and the donor remain quenched when not incorporated into the amplification product.

69. (Previously Presented) The method of claim 68 wherein said quenching is achieved following anyone of:

- a. at least the oligonucleotide labeled with the acceptor provided in a hair-pin quenched configuration, where the acceptor is provided quenched with a quencher or both the donor as well as the acceptor labeled oligonucleotides are provided in hair-pin quenched configuration so that both the donor and the acceptor moieties are provided quenched with two separate quenchers, the quenchers are provided on the same oligonucleotides and attached at or near the respective 5' ends, the quencher and the acceptor or the donor are on two opposite strands of the stem structure and part of the same oligonucleotide; and in the event of formation of hair-pin stem structure the nucleotide to which the donor or the acceptor moiety is attached is complementary and opposite to the nucleotide to which the quencher

is attached or the nucleotide to which the donor or the acceptor moiety is attached and the complement of the nucleotide to which the quencher is attached are within five nucleotides, the donor labeled and or acceptor labeled hair-pin quenched oligonucleotides remain quenched when not incorporated into the amplification product;

- b. using additional one or two oligonucleotides as the case may be each being labeled separately at or near 5' end with suitable quencher for the acceptor or the donor MET moiety such that one member of the quencher labeled additional oligonucleotide is fully or partly complementary to the acceptor labeled oligonucleotide resulting in quenching of the acceptor when the acceptor labeled oligonucleotide is not incorporated into the amplification product and the second member of the quencher labeled additional oligonucleotide is fully or partly complementary to the donor labeled oligonucleotide resulting in quenching of the donor when the donor labeled oligonucleotide is not incorporated into the amplification product ; and
- c. by providing the acceptor labeled oligonucleotide linked to another suitable oligonucleotide complementary partly or fully to this acceptor labeled oligonucleotide and labeled with a quencher at or near its 5' end through a non-nucleotide organic linker or linker and spacer or by providing both the acceptor and donor labeled oligonucleotides linked to two separate additional suitable oligonucleotides fully or partly complementary to the acceptor and donor labeled oligonucleotides respectively through non-nucleotide organic linkers or linkers and spacers and labeled at or near their 5' ends with two quenchers respectively so that the quenchers can quench the acceptor and the donor when the acceptor and the donor labeled oligonucleotides are not incorporated into the amplification product.

70. (Previously Presented) The method of claim 63 wherein a first oligonucleotide primer pair selected to amplify a first segment of the target nucleic acid is used at appropriate concentrations, a second oligonucleotide primers selected to amplify a second segment of the first segment at appropriate concentration used in nested PCR when the second oligonucleotide primer pair is any of the labeled oligonucleotide primer pairs of claim 65.

71. (Previously Presented) The method of claim 63 wherein a first oligonucleotide primer pair selected to amplify a first segment of the target nucleic acid is used at appropriate concentration, where one of the said oligonucleotide primer pair is a first member of the primer pairs of claim 63 which can be either labeled or unlabeled, a third oligonucleotide unlabeled or suitably labeled for MET and designed to amplify a second segment of the first segment in association with the above first member is nested with signal being generated on said selective amplification of the target nucleic acid.

72. (Previously Presented) The method of claim 63, wherein said nucleic acid amplification reaction comprise any known nucleic acid amplification reactions preferably polymerase chain reaction comprising the steps of adding a polymerase, reaction buffer, deoxy nucleoside triphosphates in addition to the effective amounts of amplification primers to the sample, cycling the sample, between at least a denaturation temperature and an annealing temperature, exciting the reaction mixture with the donor exciting radiation or light, measuring the emission of the acceptor MET moiety, optionally that of the donor.

73. (Previously Presented) The method of claim 63, wherein said step of amplifying the target sequence comprise a nucleic acid amplification reaction carried out using one labeled oligonucleotide as one of the two amplification primers of the target sequence amplification reaction along with the other unlabeled primer and a third labeled oligonucleotide for the amplification product, the said labeled oligonucleotide primer being labeled at or near 3' end with a donor or an acceptor MET moiety of a donor-acceptor MET pair and the said third oligonucleotide being labeled at or near 3' end respectively with an acceptor or donor MET moiety of the above MET pair such that upon successful amplification of the target sequence

the labeled primer gets incorporated into one of the two strands of the amplification product and the third labeled oligonucleotide hybridizes to this strand of the amplification product into which the labeled oligonucleotide primer get incorporated thus bringing the donor and the acceptor MET moieties within a MET distance 0-20 nucleotides of one another preferably between 1-10/15 resulting in MET between the two moieties; the above said amplification reaction comprising the steps of adding polymerase, reaction buffer, deoxy nucleoside triphosphates in addition to the effective amounts of the amplification primers to the samples, cycling the sample between at least a denaturation temperature and an elongation temperature, exciting the reaction mixture with the donor exciting radiation or light, measuring the emission of the acceptor MET moiety and optionally the reduction in donor emission, thus allowing detection of nucleic acid target without creating inhibition to amplification reaction and signal measurement without loss of signal.

74. (Previously Presented) The method of claim 63, wherein

- a. at least the oligonucleotide labeled with the acceptor is provided in quenched configuration such that the acceptor remains quenched when the acceptor labeled oligonucleotide is not incorporated into or not hybridized to the amplification product, thus reducing the background and remains unquenched in open configuration of the oligonucleotide producing signal when incorporated into or hybridized to the amplification product;
- b. the amplified sample is illuminated with light absorbed by the donor MET moiety; and
- c. monitoring the sensitized emission from the acceptor and optionally emission from donor of the MET pair moieties.

75. (Previously Presented) The method of claim 63, wherein a first oligonucleotide of linear or hair-pin configuration labeled with a donor moiety at or near preferably near its 3' end and

a second oligonucleotide singly labeled at or near its 3' end with an acceptor moiety capable of absorbing the energy or light emitted by the donor, where the acceptor is selected from a fluorophore or a quencher preferably a quencher including DABCYL or its analogue or nanogold particle black hole quencher, the donor moiety of the first oligonucleotide kept quenched when the first oligonucleotide is not incorporated into the amplification product either by providing a third oligonucleotide fully or partly complementary to the first oligonucleotide separately or linked to first oligonucleotide through an organic non-nucleotide linker and labeled at or near its 5' end with a quencher moiety or by providing the first donor labelled oligonucleotide as hair-pin oligonucleotide with a quencher at or near its 5' ends so configured that the quencher comes in close proximity to the donor moiety in its stem structure, the quencher is selected to be capable of absorbing the energy or light emitted by the donor, and selected to be a fluorophore or a non-radiative quencher preferably a quencher including DABCYL or its analogue, nanogold particle, black hole quencher, and not excluding others, the first and second oligonucleotides are the two primers of nucleic acid amplification reaction and are used such that the emission of the donor is quenched by the quencher/acceptor on the second oligonucleotide only in case of formation of primer dimer but in case of specific amplification product formation the above said quencher/acceptor of second oligonucleotide remains at least 10 bases away from the donor moiety incorporated into the amplification product through the first oligonucleotide and at the same time the quencher of first oligonucleotides remains at least 10 bases away from the donor moiety incorporated into the amplification product through the first oligonucleotides thus allowing the donor moiety to emit its characteristic energy or light and signal generation for the detection or quantitation of a target nucleic acid sequence with increased signal to noise.

76. (Previously Presented) The method of claim 63, where a first oligonucleotide labeled with a donor-1 moiety at or near preferably near its 3' end and a second oligonucleotide singly labeled at or near its 3' end with an acceptor moiety capable of absorbing the energy or light emitted by the donor-1 and a third oligonucleotide singly labeled with a donor-2 moiety at or near its 5' end are provided, the donor-1 is capable of absorbing the energy or light emitted by the donor-2, the third oligonucleotide is fully or partly complementary as long as the

complementarity is maintained such that the donor-2 moiety remains quenched by the donor-1 moiety when the first oligonucleotide is not incorporated into the amplification product ; on incorporation of the first oligonucleotide and the second oligonucleotide into the amplification product the donor-2 moiety labeled third oligonucleotide gets separated from the donor-1 labeled first oligonucleotide and the emission of the donor-2 moiety is measured.

77. (Previously Presented) The method of claim 63, wherein said oligonucleotides are of the length 10 to 40 bases preferably 15 -30 bases and the said hair-pin oligonucleotides comprise anyone of the following:

- a. a first oligonucleotide 10 – 40 bases long preferably 15 – 30 bases long fully complementary to the target nucleic acid sequence at the 5' end of which is attached a 5 – 9 bases long second oligonucleotide which may or may not be partially or fully complementary to the target sequence but fully complementary to the 3' end of the first oligonucleotide thus forming a stem and loop structure;
- b. a first oligonucleotide of length between 15 – 40 preferably 15 – 30 bases fully complementary to the target nucleic acid sequence at the 5' end of which is attached a second oligonucleotide of length 2 to 12 bases and again at the 5' end of the second oligonucleotide is attached a third oligonucleotide of length 5 – 9 bases, the second and the third oligonucleotide may or may not be partly or fully complementary to the target nucleic acid sequence but the third oligonucleotide being fully complementary to 5 – 9 bases at or near the 3' end of the first oligonucleotide thus forming stem and loop structure;
- c. a first oligonucleotide of length between 15 – 40 bases preferably between 15 – 30 bases fully complementary to the target nucleic acid sequence at the 5' end of the said first oligonucleotide is attached a second oligonucleotide of length 5 – 9 bases and at the 3' end of the said first oligonucleotide is attached a third oligonucleotide of length 5 – 9 bases, the second and the third oligonucleotides

being fully complementary to each other, may or may not be fully or partly complementary to the target nucleic acid sequence thus forming a stem and a loop structure of said hair – pin oligonucleotide;

- d. a first oligonucleotide of length between 15 – 50 preferably 15 – 30 bases fully complementary to the target nucleic acid sequence at the 5' end of a first which is attached a second oligonucleotide of length 10 to 30 bases through a non-nucleotide organic linker the second oligonucleotide may or may not be partly or fully complementary to the target nucleic acid sequence but the second oligonucleotide being complementary to the bases at or near the 3' end of the first oligonucleotide.

78. (Previously Presented) The method of claim 63, wherein in case of quenched hair-pin, linear or otherwise oligonucleotide the nucleotide to which the donor or acceptor MET moiety is attached is either opposite or within 5 nucleotides away from the nucleotide to which the quencher for the respective donor or acceptor is attached, the donor/ acceptor MET moiety and the quencher being on two opposite stands of the stem.

79. (Previously Presented) The method of claim 63, wherein said oligonucleotides are selected from DNA or RNA or chimeric mixtures or derivatives or modified versions thereof adapted for priming the amplification reaction or hybridizing to the amplified product and are deoxy oligonucleotides, oligonucleotide or peptide nucleic acid or modified oligonucleotides, the target nucleic acid sequence being selected from genomic DNA, mRNA, RNA, cDNA, chemically synthesized DNA or RNA.

80. (Previously Presented) The method of claim 63, wherein said oligonucleotides are amplification primers (forward and reverse) of polymerase chain reaction (PCR), reverse transcription PCR (RT-PCR), allele specific PCR, methylation status PCR, *in situ* PCR, Triamplification, Nucleic acid sequence based amplification, immuno PCR and not excluding others.

81. (Previously Presented) The method of claim 63 used in real time RNA expression profiling by simultaneously quantitating large number of mRNAs or cDNAs using preferably PCR, RT – PCR, NASBA by using suitably labeled oligonucleotide primer pairs selected from individual mRNAs or cDNAs.

82. (Previously Presented) The method of claim 63 used in high throughput nucleic acid amplification reactions including PCR, RT-PCR and NASBA comprising providing first oligonucleotide amplification primer for each mRNAs or cDNAs in large number from a pool selected from the sequences near the 5' ends of individual mRNAs or cDNAs and providing as second amplification primer a single common oligonucleotide primer (common for all mRNAs or cDNAs in the pool or sample) complementary to a sequence joined or ligated to 5' end of all mRNAs or cDNAs synthesized by reverse transcription in the pool or sample prior to the subjection to the amplification reaction the oligonucleotide primers being said labeled oligonucleotides primer pairs either first oligonucleotide amplification primer is dual labeled quenched primer of the invention and the second common amplification primer is an unlabeled oligonucleotide or the first oligonucleotide amplification primer is labeled at or near preferably near 3' end with a donor or an acceptor MET moiety and the second common oligonucleotide amplification primer is labeled at or near preferably near 3' end with an acceptor or donor MET moiety respectively which can also be provided quenched.

83. (Previously Presented) The method of claim 63 used in high throughput nucleic acid amplification reactions including PCR, RT-PCR and NASBA comprising providing first oligonucleotide amplification primer for each mRNAs or cDNAs in large number from a pool selected from the sequences near the 3' or 5' ends of a restriction site of cDNAs of individual mRNAs and providing as second amplification primer a single common oligonucleotide primer (common for all mRNAs or cDNAs in the pool or sample) complementary to a sequence joined or ligated to 3' and 5' ends of the restriction fragments of all cDNAs synthesized by reverse transcription in the pool or sample prior to the

subjection to the amplification reaction the oligonucleotide primers being said labeled oligonucleotides primer pairs, either first specific oligonucleotide amplification primer is dual labeled quenched primer of the invention and the second common amplification primer is an unlabeled oligonucleotide or the first oligonucleotide amplification primer is labeled at or near preferably near 3' end with a donor or an acceptor MET moiety and the second common oligonucleotide amplification primer is labeled at or near preferably near 3' end with an acceptor or donor MET moiety respectively, which can also be provided quenched.

84. (Previously Presented) The method of claim 63 used in RNA splice variant detection, wherein the target nucleotide sequence is a mRNA or a cDNA and the labeled oligonucleotides are either amplification primers (forward and reverse) of many nucleic acid amplification reactions including polymerase chain reaction (PCR), Reverse transcription polymerase chain reaction (RT-PCR), NASBA, one from 3' end of one exon and the other from 5' end of the adjacent exon or one of the two amplification primers of many nucleic acid amplification reactions including PCR, RT-PCR from 3' end of one exon and a probe complemantary to 5'end of the adjacent exon.

85. (Previously Presented) The method of claim 63 wherein the detectable signal emitted by the acceptor MET moiety/ MET moiety is sizeable and more intense than the signal emitted by the same if there is no MET and the oligonucleotides are so designed that MET moieties come in right proximity such that MET between donor and acceptor moieties can occur and FRET is a preferred form of MET.

86. (Previously Presented) The method of claim 63 wherein the target nucleic acid sequence is an amplification product or the sequence of infectious disease agent, or genomic sequence of a human, animal, plant or any other organism mutation of which is implicated to the presence of a disorder or disease, or a human, animal or plant genomic sequence, the presence or absence of which is implicated to a disorder or disease, or a human, animal or plant genomic sequence, the presence or absence of which is implicated to susceptibility to an infectious agent, or a plant or any living organism genomic sequence the presence or absence of which

is implicated to a genetic trait or genotyping of the plants, or the living organism, or a genomic sequence of an infectious agent, the presence or absence of which is implicated to strain typing.

87. (Previously Presented) The method of claim 63 wherein the donor and acceptor pair moieties are selected from any of the donor - acceptor MET \ FRET pairs and the donor moiety is preferably selected from the group consisting of fluorescein, carboxyfluorescein (FAM), coumarin, 5-(2' amino ethyl) amino napthlein – 1- sulphonic acid (EDANS), rhodamine, anthranilamide, Reactive Red- 4,europium and terbium chelate derivatives, a combination of an organic moiety having a large extinction coefficient of absorption and a fluorophore preferably of high quantum yield. and the said acceptor moiety is preferably selected from the group consisting of fluorescein, fluorescein derivatives like JOE and others, ethidium, texas red, eosin nitrotyrosine, malachite green, pyrene butyrate, Cy- 3 dye, Cy- 5 dye , DABCYL, DABCYL derivatives, rhodamine, rhodamine derivatives, nanogold black hole quencher and the quencher is selected from the group consisting of DABCYL and its derivatives, rhodamine, nanogold particles, black hole quencher and many other acceptor moieties.

88. (Previously Presented) The method of claim 63, wherein the detection and/ or quantitation of amplified target nucleic acid is accomplished by providing double stranded DNA binding fluorescent dye selected from the group preferably consisting of ethidium bromide, CYBER™ GREEN I, pico green, acridine orange, thiazole orange Yo PRO-1 and chromomycin A3.

89. (Previously Presented) The method of claim 63, wherein the detection and /or quantitation of amplified target nucleic acid sequences is accomplished by providing the first oligonucleotide primer being labeled with a binding moiety preferably selected from biotin, magnetic particle and microsphere and a hapten or attached to an anchor oligonucleotide directly or through a linker which can be respectively captured by streptavidin or magnet or centrifugation or anti-hapten antibody, capture oligonucleotide or the like and the second

oligonucleotide primer being labeled with a signaling moiety like a fluorophore, rare earth metal chelate, biotin or a hapten, the hapten being detected utilizing antihapten antibody-enzyme conjugate, streptavidin- enzyme conjugate and enzyme substrate, and other conjugates or by using unlabeled second oligonucleotide primer and providing fluorescently labeled nucleotide in appropriate concentration in the reaction mixture.

90. (Previously Presented) The method of claim 63, wherein the higher signal to noise ratio improvement is achieved by applying hair-pin quenched labeled oligonucleotides of the invention and selecting an amplification product of the size, the size of the forward amplification primer plus the size of the reverse amplification primer plus 0-25 bases in the detection of a nucleic acid target sequence using MET/FRET between donor & acceptor moieties.

91. (Previously Presented) The method of claim 63, comprising multiplexing involving multiple pairs of MET labeled oligonucleotides for detection or quantification of multiple targets.

92. (Previously Presented) The method of claim 63 comprising heterogeneous phase detection wherein one of the two amplification primers of many amplification reactions including PCR, RT-PCR, NASBA is fixed covalently through 5' end or an internal nucleotide to a solid support through a linker and spacer, and the other amplification primer is in aqueous phase in contact with the solid phase, the said solid support to which the labeled oligonucleotide is attached is non-porous and transparent or translucent and glass or plastics like polystyrene, polyethylene, polypropylene or dextran and the like and preferably glass or glass wafer.

93. (Previously Presented) The method of claim 63 for high throughput heterogeneous phase target nucleic acid detection wherein first of the two amplification primers of many target nucleic acids for many amplification reactions including PCR, RT-PCR, NASBA are fixed covalently through 5' end or an internal nucleotide to a solid support through a linker and spacer, and the second amplification primers are in aqueous phase in contact with the solid

phase, the said solid support to which the labeled oligonucleotide is attached is non – porous and transparent or translucent and glass or plastics like polystyrene, polyethylene, polypropylene or dextran and the like and preferably glass or glass wafer.

94. (Previously Presented) The method of claim 63 used in high throughput RNA expression profiling by many nucleic acid amplification reactions including PCR, RT-PCR and NASBA not excluding others by providing first oligonucleotide amplification primer for each mRNAs or cDNAs in large number from a pool selected from the sequences near the 5' ends of individual mRNAs or cDNAs, the said first oligonucleotide primers fixed covalently through 5' end or an internal nucleotide to a solid support through a linker and spacer, and the second amplification primers are in aqueous phase in contact with the solid phase and providing as second amplification primer a single common oligonucleotide primer (common for all mRNAs or cDNAs in the pool or sample) complementary to a sequence joined or ligated to 5' end of all mRNAs or cDNAs in the pool or sample prior to the subjection to the amplification reaction the oligonucleotide primers being labeled oligonucleotides primer pairs of the invention, either first oligonucleotide amplification primer is dual labeled quenched primer of the invention and the second common amplification primer is an unlabeled oligonucleotide or the first oligonucleotide amplification primer is labeled at or near preferably near 3' end with a donor or acceptor MET moiety and the second common oligonucleotide amplification primer is labeled at or near preferably near 3' end with an acceptor or donor MET moiety respectively and also can be provided quenched.

95. (Previously Presented) The method of claim 63 used in high throughput RNA expression profiling by many nucleic acid amplification reactions including PCR, RT-PCR and NASBA not excluding others by providing first oligonucleotide amplification primer for each mRNAs or cDNAs in large number from a pool selected from the sequences near the 3' or 5' ends of a restriction site of individual mRNAs or cDNAs, the said first oligonucleotide primers fixed covalently through 5' end or an internal nucleotide to a solid support through a linker and spacer, and the second amplification primers are in aqueous phase in contact with the solid phase and providing as second amplification primer a single common oligonucleotide primer

(common for all mRNAs or cDNAs in the pool or sample) complementary to a sequence joined or ligated to the 3' and 5' ends of all mRNAs or cDNAs restriction digested fragments in the pool or sample prior to the subjection to the amplification reaction the oligonucleotide primers being labeled oligonucleotides primer pairs of the invention, either first oligonucleotide amplification primer is dual labeled quenched primer of the invention and the second common amplification primer is an unlabeled oligonucleotide or the first oligonucleotide amplification primer is labeled at or near preferably near 3' end with a donor or acceptor MET moiety and the second common oligonucleotide amplification primer is labeled at or near preferably near 3' end with an acceptor or donor MET moiety respectively and also can be provided quenched.

96. (Previously Presented) The method of claim 63 wherein one or both the primers are provided labeled with a donor or acceptor moiety and a double stranded DNA intercalating dye suitable to act as an acceptor or donor respectively at suitable concentration whereby on successful amplification donor/acceptor labeled primer/primers get incorporated into the amplification product and the double stranded DNA binding (intercalating) dye get intercalated into the amplification product thus bringing it close to the donor or acceptor moiety as the case may be and resulting in MET/FRET which can be measured, more specifically a fluorescein labeled primer and double stranded DNA binding dye Ethidium bromide are used, where fluorescein is the donor and eithidium act as is the acceptor for FRET to take place between the two.

97. (Previously Presented) The method of claim 63 used in closed tube format for detection or quantitation of one or more nucleic acid target sequences.

98. (Currently Amended) The method of claim 63 wherein the oligonucleotides used are selected from:

Seq Id 10: [[a.]] 5' – GGG GTA CTA CAG CGC CCT GA – 3'
Seq Id 19: [[b.]] 5'- GGG GTA CTA CAG CGC CCT GA –3'

|
FAM

Seq Id 13: [[c.]] 5' – GTC CTG GAA GAT GGC CAT GG – 3'
Seq Id 20: [[d.]] 5' – GTC CTG GAA GAT GGC CAT GG – 3'

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JOE

Seq Id 12: [[e.]] 5' – ATG GCC ATC GTC CTG GAA GAT GGC CAT GG – 3'

Seq Id 22: [[f.]] 5' – DABCYL-ATG GCC ATC GTC CTG GAA GAT GGC
CAT GG – 3'

|
JOE

Seq Id 23: [[g.]] 5'– DABCYL-ATG GCC ATC GTC CTG GAA GAT GGC
CAT GG –3'

|
FAM

Seq Id 24: [[h.]] 5' – GCT CAT GGC GCC TGC CTG G – 3'

|
DABCYL

Seq Id 11: [[i.]] 5'- ATG GCC ATG TCC TGG AAG ATG GCC ATG G-3'

Seq Id -21: [[j.]] 5' – GGG GTA CTA CAG CGC CCT – 3' Seq Id -21

|
FAM

Seq Id 25: [[k.]] 5' – GTC CTG GAA GAT GGC CAT GG – 3'

|
Rhod

Seq Id 26: [[l.]] 5'- GTC CTG GAA GAT GGC CAT GG – 3'

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JOE

Seq Id 29: [[m.]] 5' GGC AAT GAA AAG CCA CTT CT – 3' as a forward primer to amplify a 50 base pair segment (base position 23, 565-23, 614) of E.coli genome.

Seq Id 30: [[n.]] 5' TTA ACC GGC GAT TGA GTA CC – 3' as a reverse primer to amplify a 50 base pair segment (base position 23, 565-23, 614) of E.coli genome.

99. (Previously Presented) A kit for use in method of analogous detection and/or quantitation of target nucleic acid sequence or sequences present in a sample comprising

- a. a polymerase or polymerases
- b. at least two oligonucleotides as a pair of primers for amplification of said target sequence such that after amplification the 3' ends of said pair of primers are on two opposite strands and separated from one another by 0-25 nucleotide pairs in the final amplification product;
- c. deoxynucleotides in solution (water or buffer) or lyophilized;
- d. a reaction buffer for the nucleic acid amplification reaction.

100. (Previously Presented) The kit of claim 99 wherein the oligonucleotides as pair of primers are suitably labeled separately at or near preferably near their 3'ends with a donor or an acceptor MET/FRET moiety and contains free 3'hydroxy group for polymerase to extend, the said donor and acceptor MET moieties belonging to a molecular energy transfer pair and so configured that the donor and the acceptor moieties come close within MET/FRET distance in the amplification product and the nucleotides to which the donor and acceptor moieties are attached are 0-25 nucleotide pairs away.

101. (Previously Presented) The kit of claim 100 wherein at least the acceptor moiety of the acceptor MET moiety labeled oligonucleotide primer is provided quenched when the same is not incorporated into the amplification product or both the donor and acceptor MET moieties of the respectively labeled oligonucleotide primers are provided quenched when the

same are not incorporated into the amplification product, the above quenched oligonucleotide primers being the oligonucleotide primers of claim 69.

102. (Previously Presented) The kit of claim 99 wherein additionally positive control template and suitable MET/FRET labeled primers are also included as control for amplification reaction.

103. (Previously Presented) The kit of claim 99 wherein the first oligonucleotide is labeled near 3' end with a donor MET/FRET moiety and a double stranded DNA intercalating dye capable of absorbing energy or light emitted by the donor moiety and emitting energy or light is also provided.

104. (Previously Presented) The kit of claim 99 wherein the first oligonucleotide is labeled near 3' end with an acceptor MET/FRET moiety and a double stranded DNA intercalating dye capable of emitting energy or light on illumination is provided such that the acceptor moiety is capable of absorbing the energy or light emitted by the intercalating dye and emitting energy or light.

105. (Previously Presented) The kit of claim 99 comprising multiple oligonucleotide sets of claim for detection and/or/quantitation of multiple target sequences.

106. (Previously Presented) A kit for the detection of target nucleic acid sequences or sequences using the oligonucleotides used in the methods of claim 67 wherein the detection and /or quantitation of amplified target nucleic acid sequences is accomplished by providing the first oligonucleotide primer being labeled at or near 5'end with a binding moiety preferably biotin, or magnetic particle or microsphere or a hapten or the like or attached to an anchor oligonucleotide directly or through a linker which can be respectively captured by streptavidin or magnet or centrifugation or anti-hapten antibody, capture oligonucleotide or the like and the second oligonucleotide primer being labeled with a signaling moiety like a fluorophore, rare earth metal chelate, biotin or a hapten, the hapten being detected utilizing

antihapten antibody-enzyme conjugate, streptavidin- enzyme conjugate and enzyme substrate, and other conjugates or by using unlabeled second oligonucleotide primer and providing fluorescently labeled nucleotide in the reaction mixture in appropriate concentration.

107. (Previously Presented) A kit or kits for the detection of target nucleic acid sequences providing all or more components using the oligonucleotides for detection used in methods of claim 67 wherein the detection and/ or quantitation of amplified target nucleic acid is accomplished by providing double stranded DNA binding fluorescent dye selected from the group consisting of ethidium bromide, CYBER TM GREEN I, pico green, acridine orange, thiazole orange Yo PRO- 1 and chromomycin A3 but not excluding others.

108. (Currently Amended) The kit of claim 99 wherein the oligonucleotides used are selected from:

Seq Id 10: [[a.]] 5' – GGG GTA CTA CAG CGC CCT GA – 3'

Seq Id 19: [[b.]] 5'- GGG GTA CTA CAG CGC CCT GA –3'

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FAM

Seq Id 13: [[c.]] 5' – GTC CTG GAA GAT GGC CAT GG – 3'

Seq Id 20: [[d.]] 5' – GTC CTG GAA GAT GGC CAT GG – 3'

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Seq Id 12: [[e.]] 5' – ATG GCC ATC GTC CTG GAA GAT GGC CAT GG – 3'

Seq Id 22: [[f.]] 5' – DABCYL-ATG GCC ATC GTC CTG GAA GAT GGC CAT GG – 3'

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Seq Id 23: [[g.]] 5'– DABCYL-ATG GCC ATC GTC CTG GAA GAT GGC CAT GG –3'

|
FAM

Seq Id 24: [[h.]] 5' – GCT CAT GGC GCC TGC CTG G – 3'

|
DABCYL

Seq Id 11: [[i.]] 5'- ATG GCC ATG TCC TGG AAG ATG GCC ATG G-3'

Seq Id 21: [[j.]] 5' – GGG GTA CTA CAG CGC CCT – 3'

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FAM

Seq Id 25: [[k.]] 5' – GTC CTG GAA GAT GGC CAT GG – 3'

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Rhod

Seq Id 26: [[l.]] 5'- GTC CTG GAA GAT GGC CAT GG – 3'

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JOE

Seq Id 29: [[m.]] 5' GGC AAT GAA AAG CCA CTT CT – 3' as a forward primer to amplify a 50 base pair segment (base position 23, 565-23, 614) of E.coli genome

Seq Id 30: [[n.]] 5' TTA ACC GGC GAT TGA GTA CC – 3' as a reverse primer to amplify a 50 base pair segment (base position 23, 565-23, 614) of E.coli genome.

109. (Previously Presented) A method of manufacture of a kit for use in method of analogous detection and/or quantitation of target nucleic acid sequence or sequences present in a sample comprising

- a. providing a polymerase or polymerases
- b. providing a first oligonucleotide of sequence complementary to the nucleotide sequence flanking a target nucleotide sequence suitably labeled with a donor MET/FRET moiety at or near 3' end.
- c. providing a second oligonucleotide of sequence at 5' end of the first nucleotide sequence complementary to the nucleotide sequence flanking the target nucleotide sequence or the segment of the target nucleotide sequence suitably labeled with an acceptor MET/FRET moiety at or near 3' end.
- d. providing deoxy nucleotides in solution (water or buffer) or lyophilized.
- e. providing a reaction buffer for the nucleic acid amplification reaction.

wherein the first and the second oligonucleotide sequences comprise the two primers (forward and reverse) of many nucleic acid amplification reactions and adapted to generate a detectable signal if the two oligonucleotides get incorporated into two opposite strands of amplified product and come in right proximity an the first and second oligonucleotides are any of the quenched oligonucleotide primers of claim 63.

110. (Previously Presented) A method for high throughput RNA expression preferably for analysis of absolute quantating of mRNAs carried out in homogenous or heterogeneous phase using the method of detection/quantification of target nucleic acid sequence as claimed in claim 63.

111. (Previously Presented) The method of claim 63 for the heterogeneous mutation detection comprising two amplification primer oligonucleotides of the invention one being labeled with a donor MET moiety near 3' end and the other being labeled with an acceptor MET moiety near 3' end, carrying out target amplification reaction and thermal denaturation analysis of the amplification product or products thus amplified and the same method where the labeled oligonucleotides are also provided in quenched configuration.

112. (Previously Presented) The method of claim 63 used in high throughout nucleic acid amplification reactions including PCR, RT-PCR and not excluding others.

113. (Previously Presented) The method of claim 63 wherein the donor moiety is a combination of an organic moiety having a large extinction coefficient of absorption and a fluorophore preferably of high quantum yield and extinction coefficient.

114. (Previously Presented) The method of claim 63 wherein the higher signal to noise ratio is achieved by applying hair-pin quenched labeled oligonucleotides of the invention in ligase chain reaction.

115. (Previously Presented) The method of claim 63 wherein the higher signal to noise ratio improvement is achieved by applying hair-pin quenched or otherwise quenched labeled oligonucleotides of the invention in the detection of a nucleic acid target sequence using MET/FRET between donor and acceptor moieties on two oligonucleotides designed against one strand of the target sequence.

116. (Previously Presented) The method of claim 63 wherein one or both the amplification primers are labeled at or near 3' end with acceptor or donor moiety or moieties and one of the four deoxynucleotides is provided labeled with the donor or acceptor moiety respectively in appropriate concentrations and composition, and wherein on incorporation of the acceptor labeled primer or primers and the donor labeled nucleotide into the amplification product there is MET/FRET between the donor and the acceptor.

117. (Previously Presented) The kit of claim 99 wherein the polymerases are a reverse transcriptase, T7 RNA polymerase and a DNA polymerase.

118. (Previously Presented) A method of detection of target nucleic acid sequence, a kit used for the same and its process of manufacture substantially as herein described and illustrated with reference to examples and figures and many modifications thereof.